RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10 516,429

Source: PCT

Date Processed by STIC: 12-10-04

ENTERED

RAW SEQUENCE LISTING   DATE: 12/10/2004
PATENT APPLICATION: US/10/516,429   TIME: 14:07:18

Input Set : **A:\seqlist.txt**
Output Set: **N:\CRF4\12102004\J516429.raw**

```
 4 <110> APPLICANT: INOUE, Makoto
 5        HASEGAWA, Mamoru
 6        HIRONAKA, Takashi
 8 <120> TITLE OF INVENTION: Paramyxoviral Vectors Encoding
 9        Antibodies and Uses Thereof
11 <130> FILE REFERENCE: 50026/049001
```
C--> `13 <140> CURRENT APPLICATION NUMBER: US/10/516,429`
C--> `13 <141> CURRENT FILING DATE: 2004-11-30`
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13 <150> PRIOR APPLICATION NUMBER: PCT/JP03/07005
14 <151> PRIOR FILING DATE: 2003-06-03
16 <150> PRIOR APPLICATION NUMBER: 2002-161964
17 <151> PRIOR FILING DATE: 2002-06-03
19 <160> NUMBER OF SEQ ID NOS: 63
21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 10
25 <212> TYPE: DNA
26 <213> ORGANISM: Sendai virus
28 <400> SEQUENCE: 1
29 ctttcaccct                                              10
31 <210> SEQ ID NO: 2
32 <211> LENGTH: 15
33 <212> TYPE: DNA
34 <213> ORGANISM: Sendai virus
36 <400> SEQUENCE: 2
37 tttttcttac tacgg                                        15
39 <210> SEQ ID NO: 3
40 <211> LENGTH: 18
41 <212> TYPE: DNA
42 <213> ORGANISM: Artificial Sequence
44 <220> FEATURE:
45 <223> OTHER INFORMATION: a spacer sequence
47 <400> SEQUENCE: 3
48 cggccgcaga tcttcacg                                     18
50 <210> SEQ ID NO: 4
51 <211> LENGTH: 18
52 <212> TYPE: DNA
53 <213> ORGANISM: Artificial Sequence
55 <220> FEATURE:
56 <223> OTHER INFORMATION: a spacer sequence
58 <400> SEQUENCE: 4
59 atgcatgccg gcagatga                                     18
61 <210> SEQ ID NO: 5
```

RAW SEQUENCE LISTING   DATE: 12/10/2004
PATENT APPLICATION: US/10/516,429   TIME: 14:07:18

Input Set : **A:\seqlist.txt**
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```
 62 <211> LENGTH: 18
 63 <212> TYPE: DNA
 64 <213> ORGANISM: Artificial Sequence
 66 <220> FEATURE:
 67 <223> OTHER INFORMATION: a primer for amplifying Sendai virus genome
 68       fragment
 70 <400> SEQUENCE: 5
 71 gttgagtact gcaagagc                                              18
 73 <210> SEQ ID NO: 6
 74 <211> LENGTH: 42
 75 <212> TYPE: DNA
 76 <213> ORGANISM: Artificial Sequence
 78 <220> FEATURE:
 79 <223> OTHER INFORMATION: a primer for amplifying Sendai virus genome
 80       fragment
 82 <400> SEQUENCE: 6
 83 tttgccggca tgcatgtttc ccaaggggag agttttgcaa cc                  42
 85 <210> SEQ ID NO: 7
 86 <211> LENGTH: 18
 87 <212> TYPE: DNA
 88 <213> ORGANISM: Artificial Sequence
 90 <220> FEATURE:
 91 <223> OTHER INFORMATION: a primer for amplifying Sendai virus genome
 92       fragment
 94 <400> SEQUENCE: 7
 95 atgcatgccg gcagatga                                             18
 97 <210> SEQ ID NO: 8
 98 <211> LENGTH: 21
 99 <212> TYPE: DNA
100 <213> ORGANISM: Artificial Sequence
102 <220> FEATURE:
103 <223> OTHER INFORMATION: a primer for amplifying Sendai virus genome
104       fragment
106 <400> SEQUENCE: 8
107 tgggtgaatg agagaatcag c                                         21
109 <210> SEQ ID NO: 9
110 <211> LENGTH: 1550
111 <212> TYPE: DNA
112 <213> ORGANISM: Artificial Sequence
114 <220> FEATURE:
115 <223> OTHER INFORMATION: a gene fragment encoding V regions of antibody
116        IN-1
W--> 118 <221> NAME/KEY: CDS
     119 <222> LOCATION: (18)...(749)
W--> 121 <221> CDS
     122 <222> LOCATION: (801)...(1505)
W--> 124 <400> 9
     125 gcggccgccg tacggcc atg aaa aag aca gct atc gcg att gca gtg gca    50
     126                     Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala
```

```
127                     1           5                   10
129 ctg gct ggt ttc gct acc gta gcg cag gcc gaa gtt aaa ctg cat gag    98
130 Leu Ala Gly Phe Ala Thr Val Ala Gln Ala Glu Val Lys Leu His Glu
131             15                  20                  25
133 tca ggg cct ggg ctg gta agg cct ggg act tca gtg aag ata tcc tgc   146
134 Ser Gly Pro Gly Leu Val Arg Pro Gly Thr Ser Val Lys Ile Ser Cys
135             30                  35                  40
137 aag gct tct ggc tac acc ttc act aac tac tgg cta ggt tgg gta aag   194
138 Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr Trp Leu Gly Trp Val Lys
139             45                  50                  55
141 cag agg cct gga cat gga ctt gag tgg att gga gat att tac cct gga   242
142 Gln Arg Pro Gly His Gly Leu Glu Trp Ile Gly Asp Ile Tyr Pro Gly
143 60                  65                  70                  75
145 ggt ggt tat act aac tac aat gag aag ttc aag ggc aag gcc aca ctg   290
146 Gly Gly Tyr Thr Asn Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu
147             80                  85                  90
149 act gca gac aca tcc tcc agc act gcc tac atg cag ctc agt agc ctg   338
150 Thr Ala Asp Thr Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu
151             95                  100                 105
153 aca tct gag gac tct gct gtc tat ttc tgt gca aga ttt tac tac ggt   386
154 Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Phe Tyr Tyr Gly
155             110                 115                 120
157 agt agc tac tgg tac ttc gat gtc tgg ggc caa ggc acc acg gtc acc   434
158 Ser Ser Tyr Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr Val Thr
159             125                 130                 135
161 gtc tcc tca gca aag acc act cct ccg tct gtt tac cct ctg gct cct   482
162 Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro
163 140                 145                 150                 155
165 ggt tct gcg gct cag act aac tct atg gtg act ctg gga tgc ctg gtc   530
166 Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val
167             160                 165                 170
169 aag ggc tat ttc cct gag cca gtg aca gtg acc tgg aac tct gga tcc   578
170 Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser
171             175                 180                 185
173 ctg tcc agc ggt gtg cac acc ttc cca gct gtc ctg caa tct gac ctc   626
174 Leu Ser Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu
175             190                 195                 200
177 tac act ctg agc agc tca gtg act gtc ccc tcc agc acc tgg ccc agc   674
178 Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser
179             205                 210                 215
181 gag acc gtc acc tgc aac gtt gcc cac ccg gct tct agc acc aaa gtt   722
182 Glu Thr Val Thr Cys Asn Val Ala His Pro Ala Ser Ser Thr Lys Val
183 220                 225                 230                 235
185 gac aag aaa atc gta ccg cgc gac tgc taaccgtagt aagaaaact          769
186 Asp Lys Lys Ile Val Pro Arg Asp Cys
187             240
189 tagggtgaaa gttcatcgcg gccgtacggc c atg aaa caa agc act att gca    821
190                                     Met Lys Gln Ser Thr Ile Ala
191                                     245                 250
```

```
193 ctg gca ctc tta ccg tta ctg ttt acc cct gtg aca aaa gcc gac atc   869
194 Leu Ala Leu Leu Pro Leu Leu Phe Thr Pro Val Thr Lys Ala Asp Ile
195             255                 260                 265
197 gag ctc acc cag tct cca gca atc atg gct gca tct gtg gga gaa act   917
198 Glu Leu Thr Gln Ser Pro Ala Ile Met Ala Ala Ser Val Gly Glu Thr
199             270                 275                 280
201 gtc acc atc aca tgt gga gca agt gag aat att tac ggt gct tta aat   965
202 Val Thr Ile Thr Cys Gly Ala Ser Glu Asn Ile Tyr Gly Ala Leu Asn
203     285                 290                 295
205 tgg tat cag cgg aaa cag gga aaa tct cct cag ctc ctg atc tat ggt  1013
206 Trp Tyr Gln Arg Lys Gln Gly Lys Ser Pro Gln Leu Leu Ile Tyr Gly
207 300                 305                 310                 315
209 gca acc aac ttg gca gat ggc atg tca tcg agg ttc agt ggc agt gga  1061
210 Ala Thr Asn Leu Ala Asp Gly Met Ser Ser Arg Phe Ser Gly Ser Gly
211             320                 325                 330
213 tct ggt aga cag tat tct ctc aag atc agt agc ctg cat cct gac gat  1109
214 Ser Gly Arg Gln Tyr Ser Leu Lys Ile Ser Ser Leu His Pro Asp Asp
215             335                 340                 345
217 gtt gca acg tat tac tgt caa aat gtg tta agt act cct cgg acg ttc  1157
218 Val Ala Thr Tyr Tyr Cys Gln Asn Val Leu Ser Thr Pro Arg Thr Phe
219     350                 355                 360
221 gga gct ggg acc aag ctc gag ctg aag cgc gct gat gct gca ccg act  1205
222 Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Ala Asp Ala Ala Pro Thr
223     365                 370                 375
225 gta tcc atc ttc cca cca tcc agt gag cag tta aca tct gga ggt gcc  1253
226 Val Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala
227 380                 385                 390                 395
229 tca gtc gtg tgc ttc ttg aac aac ttc tac ccc aaa gac atc aat gtc  1301
230 Ser Val Val Cys Phe Leu Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val
231             400                 405                 410
233 aag tgg aag att gat ggc agt gaa cga caa aat ggc gtc ctg aac agt  1349
234 Lys Trp Lys Ile Asp Gly Ser Glu Arg Gln Asn Gly Val Leu Asn Ser
235             415                 420                 425
237 tgg act gat cag gac agc aaa gac agc acc tac agc atg agc agc acc  1397
238 Trp Thr Asp Gln Asp Ser Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr
239     430                 435                 440
241 ctc acg ttg acc aag gac gag tat gaa cga cat aac agc tat acc tgt  1445
242 Leu Thr Leu Thr Lys Asp Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys
243     445                 450                 455
245 gag gcc act cac aag aca tca act tca ccc att gtc aag agc ttc aac  1493
246 Glu Ala Thr His Lys Thr Ser Thr Ser Pro Ile Val Lys Ser Phe Asn
247 460                 465                 470                 475
249 agg aat gag tgt tagtccgtag taagaaaac ttagggtgaa agttcatgcg  1545
250 Arg Asn Glu Cys
253 gccgc                                                            1550
255 <210> SEQ ID NO: 10.
256 <211> LENGTH: 244
257 <212> TYPE: PRT
258 <213> ORGANISM: Artificial Sequence
```

```
260 <220> FEATURE:
261 <223> OTHER INFORMATION: an immunoglobulin IN-1 heavy chain
263 <400> SEQUENCE: 10
264 Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
265 1               5                   10              15
266 Thr Val Ala Gln Ala Glu Val Lys Leu His Glu Ser Gly Pro Gly Leu
267             20              25              30
268 Val Arg Pro Gly Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr
269         35              40              45
270 Thr Phe Thr Asn Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His
271     50              55              60
272 Gly Leu Glu Trp Ile Gly Asp Ile Tyr Pro Gly Gly Gly Tyr Thr Asn
273 65              70              75              80
274 Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Thr Ser
275             85              90              95
276 Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser
277             100             105             110
278 Ala Val Tyr Phe Cys Ala Arg Phe Tyr Tyr Gly Ser Ser Tyr Trp Tyr
279         115             120             125
280 Phe Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Ala Lys
281     130             135             140
282 Thr Thr Pro Pro Ser Val Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln
283 145             150             155             160
284 Thr Asn Ser Met Val Thr Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro
285             165             170             175
286 Glu Pro Val Thr Val Thr Trp Asn Ser Gly Ser Leu Ser Ser Gly Val
287             180             185             190
288 His Thr Phe Pro Ala Val Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser
289         195             200             205
290 Ser Val Thr Val Pro Ser Ser Thr Trp Pro Ser Glu Thr Val Thr Cys
291     210             215             220
292 Asn Val Ala His Pro Ala Ser Ser Thr Lys Val Asp Lys Lys Ile Val
293 225             230             235             240
294 Pro Arg Asp Cys
298 <210> SEQ ID NO: 11
299 <211> LENGTH: 235
300 <212> TYPE: PRT
301 <213> ORGANISM: Artificial Sequence.
303 <220> FEATURE:
304 <223> OTHER INFORMATION: an immunoglobulin IN-1 light chain
306 <400> SEQUENCE: 11
307 Met Lys Gln Ser Thr Ile Ala Leu Ala Leu Leu Pro Leu Leu Phe Thr
308 1               5                   10              15
309 Pro Val Thr Lys Ala Asp Ile Glu Leu Thr Gln Ser Pro Ala Ile Met
310             20              25              30
311 Ala Ala Ser Val Gly Glu Thr Val Thr Ile Thr Cys Gly Ala Ser Glu
312             35              40              45
313 Asn Ile Tyr Gly Ala Leu Asn Trp Tyr Gln Arg Lys Gln Gly Lys Ser
314     50              55              60
```

VERIFICATION SUMMARY
PATENT APPLICATION: **US/10/516,429**

DATE: 12/10/2004
TIME: 14:07:19

Input Set : **A:\seqlist.txt**
Output Set: **N:\CRF4\12102004\J516429.raw**

L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:118 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:121 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9
L:124 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9